Amendments to the Specification:

Please amend the paragraph on page 5 starting at line 28 as follows:

Figure 1 is a diagrammatic representation showing the structural organization of HBV surface antigen.

~~(A)~~ **Figure 1A** shows ~~The~~ the location of the major hydrophilic loop covering the conserved "a" determinant (adapted from Chen et al. (7)). The size of the full-length HBsAg in amino acid residues is indicated (1-400). Positions of preS1 (1-118), preS2 (119-174) and the major HBsAg (175-400) are indicated blow the box. The position of the major hydrophobic loop in relation to the full-length HBsAg is also indicated. The corresponding position of the major hydrophilic loop within the major HBsAg (SHBsAg) is from amino acid 100 to 160, and the conserved "a" determinant from 124 to 147 within SHBsAg.

~~(B)~~ **Figure 1B** shows ~~The~~ the genomic location of the region coding for SHBsAg. The positions of 5'- and 3'-end of the coding region are indicated below the box (nt 156 and 835 of the HBV genome, respectively, the position 1 being defined as the first A nucleotide of the *EcoRI* site – GAATTC ~~(<400>3~~ SEQ ID NO: 3) of the wild-type HBV with Z35717 as its GenBank accession number). The positions of the primer oligonucleotides provided in the present invention ~~(<400>1~~ SEQ ID NO: 1 and ~~<400>2~~ SEQ ID NO: 2) are also indicated below the box (starting from nt 456 and 689 of the HBV genome, respectively). The size of PCR-amplified DNA fragment utilizing the primer oligonucleotides of the present invention ~~(<400>1~~ SEQ ID NO: 1 and ~~<400>2~~ SEQ ID NO: 2) is 233 base pairs (bp), as indicated below the box.

Please amend the paragraph on page 6 starting at line 9 as follows:

Figure 2 is a photographic representation showing the electrophoresis pattern of PCR-amplified HBV fragment from test sample, negative for HBsAg by immune-based diagnostic kits but positive for anti-HBc and anti-HBs, utilizing the primer oligonucleotides provided in the present invention ~~(<400>1~~ SEQ ID NO: 1 and ~~<400>2~~ SEQ ID NO: 2). Indicated in *lane 4* are migration positions of molecular size markers (100 bp ladder, MBI Fermentas). *Lane 1* correponds to the first test sample in Table ~~1~~ 2; *lane 2* corresponds to the second test sample in Table ~~1~~ 2. *Lanes 6* and *9* correspond to the third and fourth test samples in Table ~~1~~ 2, respectively. No amplification products are seen in lanes 3, 5, 7 and 8 that represent test samples displaying similar viral markers (negative for HBsAg, positive for anti-HBc and anti-HBs).